SEQUENCE LISTING

<110>   Sanjay Bhanot
Kenneth W. Dobie

<120>   MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION

<130>   RTS-0678US

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<223>   Antisense Oligonucleotide

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<220>

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APP_ID=10643801

<222> (231)...(1397)

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ccgggacccc tgtgctctgc gcgaagccct ggccccgggg gccggggcat gggccagggg     180

cgcggggtga agcggcttcc cgcggggccg tgactgggcg ggcttcagcc atg aag        236
                                                          Met Lys
                                                            1
```

```
acc ctc ata gcc gcc tac tcc ggg gtc ctg cgc ggc gag cgt cag gcc      284
Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu Arg Gln Ala
             5                  10                  15
```

```
gag gct gac cgg agc cag cgc tct cac gga gga cct gcg ctg tcg cgc      332
Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro Ala Leu Ser Arg
     20                  25                  30
```

```
gag ggg tct ggg aga tgg ggc act gga tcc agc atc ctc tcc gcc ctc      380
Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser Ala Leu
 35                  40                  45                  50
```

```
cag gac ctc ttc tct gtc acc tgg ctc aat agg tcc aag gtg gaa aag      428
Gln Asp Leu Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val Glu Lys
                 55                  60                  65
```

```
cag cta cag gtc atc tca gtg ctc cag tgg gtc ctg tcc ttc ctt gta      476
Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe Leu Val
                 70                  75                  80
```

```
ctg gga gtg gcc tgc agt gcc atc ctc atg tac ata ttc tgc act gat      524
Leu Gly Val Ala Cys Ser Ala Ile Leu Met Tyr Ile Phe Cys Thr Asp
             85                  90                  95
```

```
tgc tgg ctc atc gct gtg ctc tac ttc act tgg ctg gtg ttt gac tgg      572
Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Val Phe Asp Trp
 100                 105                 110
```

```
aac aca ccc aag aaa ggt ggc agg agg tca cag tgg gtc cga aac tgg      620
Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg Asn Trp
115                 120                 125                 130
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```
gct gtg tgg cgc tac ttt cga gac tac ttt ccc atc cag ctg gtg aag      668
Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys
                 135                 140                 145
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aca cac aac ctg ctg acc acc agg aac tat atc ttt gga tac cac ccc      716
Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro
             150                 155                 160
```

```
cat ggt atc atg ggc ctg ggt gcc ttc tgc aac ttc agc aca gag gcc      764
His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala
             165                 170                 175
```

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aca gaa gtg agc aag aag ttc cca ggc ata cgg cct tac ctg gct aca      812
Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr
     180                 185                 190
```

```
ctg gca ggc aac ttc cga atg cct. gtg ttg agg gag tac ctg atg tct    860
Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
195                 200                 205                 210

gga ggt atc tgc cct gtc agc cgg gac acc ata gac tat ttg ctt tca    908
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu Ser
                    215                 220             .       225

aag aat ggg agt ggc aat gct atc atc atc gtg gtc ggg ggt gcg gct    956
Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly Ala Ala
                230                 235                 240

gag tct ctg agc tcc atg cct ggc aag aat gca gtc acc ctg cgg aac·   1004
Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu Arg Asn
        245                 250                 255

cgc aag ggc ttt gtg aaa ctg gcc ctg cgt cat gga gct gac ctg gtt   1052
Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp Leu Val
    260         `       265                 270

ccc atc tac tcc ttt gga gag aat gaa gtg tac aag cag gtg atc ttc   1100
Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val Ile Phe
275                 280                 285                 290

gag gag ggc tcc tgg ggc cga tgg gtc cag aag aag ttc cag aaa tac   1148
Glu Glu Gly Ser Trp Gly Arg Trp Val Gln Lys Lys Phe Gln Lys Tyr
                295                 300                 305

att ggt ttc gcc cca tgc atc ttc cat ggt cga ggc ctc ttc tcc tcc   1196
Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe Ser Ser
                310                 315                 320

gac acc tgg ggg ctg gtg ccc tac tcc aag ccc atc acc act gtt gtg   1244
Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr Val Val
        325                 330                 335

gga gag ccc atc acc atc ccc aag ctg gag cac cca acc cag caa gac   1292
Gly Glu Pro Ile Thr Ile Pro Lys Leu Glu His Pro Thr Gln Gln Asp
    340                 345                 350

atc gac ctg tac cac acc atg tac atg gag gcc ctg gtg aag ctc ttc   1340
Ile Asp Leu Tyr His Thr Met Tyr Met Glu Ala Leu Val Lys Leu Phe
355                 360                 365                 370

gac aag cac aag acc aag ttc ggc ctc ccg gag act gag gtc ctg gag   1388
Asp Lys His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu
                375                 380                 385

gtg aac tga gccagccttc ggggccaact ccctggagga accagctgca aatcactttt 1447
Val Asn

ttgctctgta aatttggaag tgtcatgggt gtctgtgggt tatttaaaag aaattataac 1507

aattttgcta aaccattaca atgttaggtc ttttttaaga aggaaaaagt cagtatttca 1567

agttctttca cttccagctt gccctgttct aggtggtggc taaatctggg cctaatctgg 1627

gtggctcagc taacctctct tcttcccttc ctgaagtgac aaaggaaact cagtcttctt 1687
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gtctagtcct gaaactgcag gaccagtttc tctgccaagg ggaggagttg gagagcacag   1867

ttgccccgtt gtgtgagggc agtagtaggc atctggaatg ctccagtttg atctcccttc   1927

tgccacccct acctcacccc tagtcactca tatcggagcc tggactggcc tccaggatga   1987

ggatggggggt ggcaatgaca ccctgcaggg gaaaggactg cccccccatgc accattgcag   2047

ggaggatgcc gccaccatga gctaggtgga gtaactggtt tttcttgggt ggctgatgac   2107

atggatgcag cacagactca gccttggcct ggagcacatg cttactggtg gcctcagttt   2167

accttcccca gatcctagat tctggatgtg aggaagagat ccctcttcag aagggggcctg   2227

gccttctgag cagcagatta gttccaaagc aggtggcccc cgaacccaag cctcactttt   2287

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ttatctcttg atgagatcat tgcaccatgt cagactttttg tatatgcctt gaaaataaat   2407

gaaagtgaga atccaaaaaa aaaaaaaaaa aa                                   2439


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<223>    PCR Primer

<400>    6
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<223>   PCR Probe

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gaaggtgaag gtcggagtc                                                  19


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gaagatggtg atgggatttc                                                 20


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agccctggcc ccggcggccg gggcatgggt caggggcgcg gcgtgaggcg gctttctgca      180

cggccgtgac gtgcattggc ttcagc atg aag acc ctc atc gcc gcc tac tcc      233
                             Met Lys Thr Leu Ile Ala Ala Tyr Ser
                              1               5

ggg gtc ctg cgg ggt gag cgt cgg gcg gaa gct gcc cgc agc gaa aac      281
Gly Val Leu Arg Gly Glu Arg Arg Ala Glu Ala Ala Arg Ser Glu Asn
 10              15                  20                  25

aag aat aaa gga tct gcc ctg tca cgc gag ggg tct ggg cga tgg ggc      329
Lys Asn Lys Gly Ser Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly
                30                  35                  40

act ggc tcc agc atc ctc tca gcc ctc caa gac atc ttc tct gtc acc      377
Thr Gly Ser Ser Ile Leu Ser Ala Leu Gln Asp Ile Phe Ser Val Thr
                45                  50                  55

tgg ctc aac aga tct aag gtg gaa aaa cag ctg cag gtc atc tca gta      425
Trp Leu Asn Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val
            60                  65                  70

cta caa tgg gtc cta tcc ttc ctg gtg cta gga gtg gcc tgc agt gtc      473
Leu Gln Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Val
        75                  80                  85

atc ctc atg tac acc ttc tgc aca gac tgc tgg ctg ata gct gtg ctc      521
Ile Leu Met Tyr Thr Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 90                  95                 100                 105

tac ttc acc tgg ctg gca ttt gac tgg aac acg ccc aag aaa ggt ggc      569
Tyr Phe Thr Trp Leu Ala Phe Asp Trp Asn Thr Pro Lys Lys Gly Gly
                110                 115                 120

agg aga tcg cag tgg gtg cga aac tgg gcc gtg tgg cgc tac ttc cga      617
Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr Phe Arg
                125                 130                 135

gac tac ttt ccc atc cag ctg gtg aag aca cac aac ctg ctg acc acc      665
Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu Leu Thr Thr
                140                 145                 150

agg aac tat atc ttt gga tac cac ccc cat ggc atc atg ggc ctg ggt      713
Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Met Gly Leu Gly
            155                 160                 165

gcc ttc tgt aac ttc agc aca gag gct act gaa gtc agc aag aag ttt      761
Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu Val Ser Lys Lys Phe
170                 175                 180                 185

cct ggc ata agg ccc tat ttg gct acg ttg gct ggt aac ttc cgg atg      809
Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu Ala Gly Asn Phe Arg Met
                190                 195                 200

cct gtg ctt cgc gag tac ctg atg tct gga ggc atc tgc cct gtc aac      857
Pro Val Leu Arg Glu Tyr Leu Met Ser Gly Gly Ile Cys Pro Val Asn
            205                 210                 215

cga gac acc ata gac tac ttg ctc tcc aag aat ggg agt ggc aat gct      905
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Arg Asp Thr Ile Asp Tyr Leu Leu Ser Lys Asn Gly Ser Gly Asn Ala
    220                 225                 230

atc atc atc gtg gtg gga ggt gca gct gag tcc ctg agc tcc atg cct      953
Ile Ile Ile Val Val Gly Gly Ala Ala Glu Ser Leu Ser Ser Met Pro
        235                 240                 245

ggc aag aac gca gtc acc ctg aag aac cgc aaa ggc ttt gtg aag ctg     1001
Gly Lys Asn Ala Val Thr Leu Lys Asn Arg Lys Gly Phe Val Lys Leu
250                 255                 260                 265

gcc ctg cgc cat gga gct gat ctg gtt ccc act tat tcc ttt gga gag     1049
Ala Leu Arg His Gly Ala Asp Leu Val Pro Thr Tyr Ser Phe Gly Glu
                270                 275                 280

aat gag gta tac aag cag gtg atc ttt gag gag ggt tcc tgg ggc cga     1097
Asn Glu Val Tyr Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg
                285                 290                 295

tgg gtc cag aag aag ttc cag aag tat att ggt ttc gcc ccc tgc atc     1145
Trp Val Gln Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile
        300                 305                 310

ttc cat ggc cga ggc ctc ttc tcc tct gac acc tgg ggg ctg gtg ccc     1193
Phe His Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro
        315                 320                 325

tac tcc aag ccc atc acc acc gtc gtg ggg gag ccc atc act gtc ccc     1241
Tyr Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Val Pro
330                 335                 340                 345

aag ctg gag cac ccg acc cag aaa gac atc gac ctg tac cat gcc atg     1289
Lys Leu Glu His Pro Thr Gln Lys Asp Ile Asp Leu Tyr His Ala Met
                350                 355                 360

tac atg gag gcc ctg gtg aag ctc ttt gac aat cac aag acc aaa ttt     1337
Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Asn His Lys Thr Lys Phe
                365                 370                 375

ggc ctt cca gag act gag gtg ctg gag gtg aac tga cccagccctc          1383
Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn
        380                 385

gcgtgccagc tcctgggagg gacgactgca gatccttttc taccgagttc ttgagtgcat    1443

tttgttctgt aaatttggaa gcgtcatggg tgtctgtggg ttatttaaaa gaaattataa    1503

tgtgttaaac cattgcaatg ttagatgttt ttttaagaag ggaagagtca gtattttaag    1563

ctcacttcta gtgtgtcctg ctcaaggtgg aggctgatat ttatgggcct tggtggtttc    1623

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gggtagataa catctggact gcccggcttg ggtctctgct cctcaccctg ccctcttct    1863

ccaatctgag cctaccctgg cctcctgtct cctggctagg gacacggctg tcccacaggt    1923
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cacagctcag cgttgctctg gcgcatatcc tcctgagcca caccccaagt ctggtgtgag   2043

gaagggcttc tcttctcttc acagaggtgc ctggcttcct gtgcagcaca ctgggtccag   2103

gacaggaggc cccccccca aaccaagcct cacgtgtgtg cctttatgag gcgttgggag   2163

aaagctaccc tcctgtgtat tctgttttct ccatgagatt gttgtgccat gtcacacttt   2223

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<223>    PCR Primer

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<223>    PCR Primer

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<223>    PCR Probe

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gaggccacca gtaagcatgt                                                        20


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gaaaagtgag gcttgggttc                                          20


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cacacacgtg aggcttggtt                                          20


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<220>

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